

SEQUENCE LISTING

<110> Powers, Scott
Yang, Jianxin
Cutler, Gene
Tularik Inc.

<120> Novel G-Protein Coupled Receptors

<130> 018781-004720US

<140> US 09/546,986

<141> 2001-04-11

<150> US 09/524,730

<151> 2000-03-14

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<170> PatentIn Ver. 2.1

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<223> human breast cancer amplified G-protein coupled
receptor 1 (BCA-GPCR-1)

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 <223> human breast cancer amplified G-protein coupled
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 Ser Ile Val Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr
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 Ala Ala Ile Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln
 145 150 155 160
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 Ser Met Val Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn
 180 185 190
 Asn Cys Ile Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu
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 Lys Ala Phe Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe
 260 265 270
 Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser
 275 280 285
 His Glu Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro
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 Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser
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receptor 4 (BCA-GPCR-4)

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Glu Ser Asn Leu Ala Gly Phe Ile Leu Leu Gly Phe Ser Asp Tyr Ala
30 35 40

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Gln Leu Gln Lys Val Leu Phe Val Leu Ile Leu Ile Leu Tyr Leu Leu
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Thr Ile Leu Gly Asn Thr Thr Ile Ile Leu Val Ser Arg Leu Glu Pro
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Lys Leu His Met Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu
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Tyr Arg Cys Phe Thr Ser Ser Val Ile Pro Gln Leu Leu Val Asn Leu
90 95 100 105

tgg gaa ccc atg aaa act atc gcc tat ggt ggc tgt ttg gtt cac ctt 388
Trp Glu Pro Met Lys Thr Ile Ala Tyr Gly Gly Cys Leu Val His Leu
110 115 120

tac aac tcc cat gcc ctg gga tcc act gag tgc gtc ctc ccg gct ctg 436
Tyr Asn Ser His Ala Leu Gly Ser Thr Glu Cys Val Leu Pro Ala Leu
125 130 135

atg tcc tgt gac cgc tat gtg gct gtc tgc cgt cct ctc cat tac act 484
Met Ser Cys Asp Arg Tyr Val Ala Val Cys Arg Pro Leu His Tyr Thr
140 145 150

gtc tta atg cat atc cat ctc tgc atg gcc ttg gca tct atg gca tgg 532
Val Leu Met His Ile His Leu Cys Met Ala Leu Ala Ser Met Ala Trp
155 160 165

ctc agt gga ata gcc acc acc ctg gta cag tcc acc ctc acc ctg cag	580
Leu Ser Gly Ile Ala Thr Thr Leu Val Gln Ser Thr Leu Thr Leu Gln	
170 175 180 185	
ctg ccc ttc tgt ggg cat cgc caa gtg gat cat ttc atc tgc gag gtc	628
Leu Pro Phe Cys Gly His Arg Gln Val Asp His Phe Ile Cys Glu Val	
190 195 200	
cct gtg ctc atc aag ctg gct tgt gtg ggc acc acg ttt aac gag gct	676
Pro Val Leu Ile Lys Leu Ala Cys Val Gly Thr Thr Phe Asn Glu Ala	
205 210 215	
gag ctt ttt gtg gct agt atc ctt ttc ctt ata gtg cct gtc tca ttc	724
Glu Leu Phe Val Ala Ser Ile Leu Phe Leu Ile Val Pro Val Ser Phe	
220 225 230	
atc ctg gtc tcc tct ggc tac att gcc cac gca gtg ttg agg att aag	772
Ile Leu Val Ser Ser Gly Tyr Ile Ala His Ala Val Leu Arg Ile Lys	
235 240 245	
tca gct acc ggg aga cag aaa gca ttc ggg acc tgc ttc tcc cac ctg	820
Ser Ala Thr Gly Arg Gln Lys Ala Phe Gly Thr Cys Phe Ser His Leu	
250 255 260 265	
aca gtg gtc acc atc ttt tat gga acc atc atc ttc atg tat ctg cag	868
Thr Val Val Thr Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr Leu Gln	
270 275 280	
cca gcc aag agt aga tcc agg gac cag ggc aag ttt gtt tct ctc ttc	916
Pro Ala Lys Ser Arg Ser Arg Asp Gln Gly Lys Phe Val Ser Leu Phe	
285 290 295	
tac act gtg gta acc cgc atg ctt aac cct ctt att tat acc ttg agg	964
Tyr Thr Val Val Thr Arg Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
300 305 310	
atc aag gag gtg aaa ggg gca tta aag aaa gtt cta gca aag gct ctg	1012
Ile Lys Glu Val Lys Gly Ala Leu Lys Lys Val Leu Ala Lys Ala Leu	
315 320 325	
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Gly Val Asn Ile Leu	
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<212> PRT

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His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe	
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Ile Leu Leu Gly Phe Ser Asp Tyr Ala Gln Leu Gln Lys Val Leu Phe	
35 40 45	
Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr	
50 55 60	
Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr	
65 70 75 80	

Phe	Phe	Leu	Ser	His	Leu	Ser	Phe	Leu	Tyr	Arg	Cys	Phe	Thr	Ser	Ser	
				85					90					95		
Val	Ile	Pro	Gln	Leu	Leu	Val	Asn	Leu	Trp	Glu	Pro	Met	Lys	Thr	Ile	
			100					105					110			
Ala	Tyr	Gly	Gly	Cys	Leu	Val	His	Leu	Tyr	Asn	Ser	His	Ala	Leu	Gly	
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Ser	Thr	Glu	Cys	Val	Leu	Pro	Ala	Leu	Met	Ser	Cys	Asp	Arg	Tyr	Val	
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Ala	Val	Cys	Arg	Pro	Leu	His	Tyr	Thr	Val	Leu	Met	His	Ile	His	Leu	
145					150					155					160	
Cys	Met	Ala	Leu	Ala	Ser	Met	Ala	Trp	Leu	Ser	Gly	Ile	Ala	Thr	Thr	
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Leu	Val	Gln	Ser	Thr	Leu	Thr	Leu	Gln	Leu	Pro	Phe	Cys	Gly	His	Arg	
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Gln	Val	Asp	His	Phe	Ile	Cys	Glu	Val	Pro	Val	Leu	Ile	Lys	Leu	Ala	
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Leu	Phe	Leu	Ile	Val	Pro	Val	Ser	Phe	Ile	Leu	Val	Ser	Ser	Gly	Tyr	
225				230				235							240	
Ile	Ala	His	Ala	Val	Leu	Arg	Ile	Lys	Ser	Ala	Thr	Gly	Arg	Gln	Lys	
			245					250						255		
Ala	Phe	Gly	Thr	Cys	Phe	Ser	His	Leu	Thr	Val	Val	Thr	Ile	Phe	Tyr	
		260						265					270			
Gly	Thr	Ile	Ile	Phe	Met	Tyr	Leu	Gln	Pro	Ala	Lys	Ser	Arg	Ser	Arg	
	275						280				285					
Asp	Gln	Gly	Lys	Phe	Val	Ser	Leu	Phe	Tyr	Thr	Val	Val	Thr	Arg	Met	
	290					295					300					
Leu	Asn	Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Ile	Lys	Glu	Val	Lys	Gly	Ala	
305				310					315						320	
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<210> 16
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24